

# Algorithms and Models for Single-Cell Genomics

June 6 – 7, 2019

Hosted by



NSF-Simons Center for  
Multiscale Cell Fate Research  
UC Irvine



University of California, Irvine • Student Center, Pacific Ballroom ABC & D

## Day 1: Thursday, 06/06/2019

**08:00 – 08:40 Registration and Breakfast**

**08:40 – 08:45 Opening**

**Qing Nie**, Director of CMCF at UCI

**08:45 – 09:00 Introduction**

**Adam MacLean** (USC) and **Luca Pinello** (Harvard)

**09:00 – 09:25 Kieran Campbell** RESEARCH

University of British Columbia

Scalable probabilistic approaches for automating integration and alignment of single-cell genomics data

**09:25 – 09:50 Sisi Chen** RESEARCH

Caltech

Building probabilistic models of single-cell data to treat human disease

**09:50 – 10:15 Joshua Welch** RESEARCH

University of Michigan

Single-cell multi-omic integration compares and contrasts features of brain cell identity

**10:15 – 10:45 Coffee Break**

**10:45 – 11:10 Huidong Chen** SOFTWARE

Harvard Medical School

STREAM: Single-cell Trajectories Reconstruction, Exploration And Mapping of omics data

**11:10 – 12:00 Martin Hemberg** KEYNOTE

Sanger Institute

Computational tools for analysis of large collections of scRNA-seq datasets

**12:00 – 01:10 Lunch**

**01:10 – 01:35 Alison Paquette** RESEARCH

Institute for Systems Biology

A Genome Scale Transcriptional Regulatory Model of the Human Placenta

**01:35 – 02:00 Timothy Daley** RESEARCH

Stanford

Dropout-based normalization for single cell data

**02:00 – 02:25 Ken Chen** RESEARCH

UT MD Anderson Cancer Center

Tracing cellular evolution through copy number alterations

**02:25 – 02:50 Coffee Break**

**02:50 – 03:15 Chris Lester** SOFTWARE

University of Oxford

Multi-level Approximate Bayesian Computation

**03:15 – 03:40 Davit Potoyan** RESEARCH

Iowa State University

Piecewise deterministic Markov models of pluripotency

**03:40 – 04:30 Michael Stumpf** KEYNOTE

University of Melbourne

Learning Mechanistic Models from Single Cell Data

**04:30 – 06:00 Poster Session**

**06:00 – 08:00 Dinner**

## Day 2: Friday, 06/07/2019

**08:00 – 09:00 Breakfast**

**09:00 – 09:25**

**Ryan Williams** SOFTWARE

*Mount Sinai School of Medicine*  
Massively-Parallel Single-Cell Analysis

**09:25 – 09:50**

**Jianhao Peng** RESEARCH

*University of Illinois*  
Single Cell GRN Inference with Inter-Cluster Similarity Constraint

**09:50 – 10:15**

**Xu Zhou** RESEARCH

*Institute for Systems Biology*  
Constructing cell-cell interaction landscape for cell population dynamics

**10:15 – 10:45 Coffee Break**

**10:45 – 11:10**

**Rowan Brackston** RESEARCH

*Imperial College London*  
Extrinsic noise in transcription: Implications and examples

**11:10 – 12:00**

**Ben Raphael** KEYNOTE

*Princeton*  
Leveraging biological knowledge in single-cell DNA and RNA-seq analysis

**12:00 – 01:15 Lunch**

**01:15 – 01:40**

**Valentine Svensson** RESEARCH

*Caltech*  
Analysis through uncertainty quantification for complex conditions

**01:40 – 02:05**

**Shahin Mohammadi** SOFTWARE

*MIT/Broad Institute*  
A robust and reproducible framework to reconstruct cell state landscape

**02:05 – 02:30**

**Ritambhara Singh** RESEARCH

*University of Washington*  
Unsupervised manifold alignment for single-cell genomics

**02:30 – 04:00 Coffee and Poster Session**

**04:00 – 04:25**

**Ilya Korunsky** RESEARCH

*Harvard Medical School*  
Fast, sensitive, and accurate integration of single cell data with Harmony

**04:25 – 04:50**

**Kwangbom Choi** SOFTWARE

*The Jackson Laboratory*  
A hierarchical model that leverages multi-mapping reads for the quantitation of gene expression from droplet single-cell RNA sequencing data

**04:50 – 05:40**

**Elana Fertig** KEYNOTE

*Johns Hopkins*  
Transfer learning of low dimensional biological processes across cellular measurements, platforms, tissues, and species from single cell data

**05:40 – 06:00 Closing**